

Antibiogram of *Klebsiella Pneumoniae* Isolated from Various Clinical Samples of Critically Intensive Care Unit Patients: A Tertiary Care Hospital Based Study from South India

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Abstract:

Klebsiella associated infections is the emergence of multi-drug resistant strains particularly those involved in nosocomial diseases. Hence, this study has been designed to determine the isolation rate of *Klebsiella pneumoniae*, their antibiogram in various clinical samples in patients admitted in intensive care units of a tertiary care hospital. A total of 6274 clinical samples were processed during the study period. Out of which 185 (2.94%) *Klebsiella pneumoniae* isolates were identified from various clinical samples during the study period. It was isolated highest in ET secretion samples (9.73%), followed by urine (2.18%), pus (1.34%) and blood (1.02%). Imipenem (58%) & Meropenem (58%) showed highest sensitivity followed by Amikacin (52%), Gentamicin (35%). Susceptibility to 3rd generation cephalosporins and beta-lactam & betalactamase inhibitor combinations was 10%-20%. We noticed that *Klebsiella pneumoniae* resistant to a wider range of antibiotics. Both morbidity and mortality is increased when infection is caused by these drug resistant organisms.

Keywords: *Klebsiella pneumoniae*; Anti-biogram; Nosocomial diseases.

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Introduction

Klebsiella is the second most popular member of the aerobic bacterial flora of the human intestine. It is the most common causative agent of opportunistic nosocomial and community acquired infections causing a variety of infections involving urinary tract infections, pneumonia, septicaemia, wound infections and infections in the intensive care units [1]. It has even replaced *Escherichia coli* in some centers as a nosocomial pathogen. Multidrug resistant is the major concern in *Klebsiella pneumoniae* infection; it increases the morbidity and mortality rate throughout the world. Antimicrobial resistance needs to be monitored cautiously to control the spread of multidrug resistant bacteria.

Klebsiella is a Gram negative, non-motile, encapsulated, lactose fermenting, facultative anaerobe belonging to the Enterobacteriaceae family [2]. In 1883 Friedlander isolated a capsulated bacillus from the lungs of patients who had died of pneumonia [3]. This was named after him as Friedlander's bacillus. Later on this organism was given the generic name of *Klebsiella*, which is ubiquitously present and reported worldwide.

Klebsiella isolates have been steadily increasing over the past years and they

have been important sources of transferable antibiotic resistance [4]. Biochemically typical strains of *Klebsiella pneumoniae* are resistant to a wider range of antibiotics than are most *Escherichia coli* strains. They are nearly always naturally resistant to ampicillin, carbenicillin, and ticarcillin [5]. Resistance of *Klebsiella* to previously sensitive antibiotics is also increasing in the recent years due to overuse and misuse of antimicrobial agents and or natural causes. Cephalosporins, fluoroquinolones, aminoglycosides and carbapenems are effective for treating infections caused by *Klebsiella* [6,7]. However, resistance to β -lactams among clinical isolates of gram-negative bacteria is increasing worldwide [8]. It has been reported that *K. pneumoniae* is resistant to ceftizoxime, cefotaxime, ceftriaxone, and ceftazidime [9].

Of particular concern is the Extended Spectrum Beta Lactamase (ESBL) producing *Klebsiella pneumoniae* that have been steadily increasing over the past years and rapidly spreading worldwide that pose a serious threat for healthcare associated infections. Increasingly the ESBL *Klebsiella pneumoniae* are also showing co-

resistance to other antimicrobial agents like quinolones and aminoglycoside antibiotics. The ESBL-producing isolates of *K. pneumoniae* have been associated with numerous outbreaks of nosocomial infections throughout the United States of America [10], and in Asia [11]. Extended spectrum β -lactamase (ESBL) producing organisms, are now being recognized as one of the major threats to effective management of patients in medical institutions, especially in the less developed nations both morbidity and mortality is increased when infection is caused by these drug resistant organisms [12].

Therefore updated knowledge of the drug resistance pattern in a particular region is useful in clinical practice. This study has been designed to determine the isolation rate of *Klebsiella pneumoniae*, their anti-biogram in various clinical samples in patients admitted in intensive care units of a tertiary care hospital.

Materials and Methods

Study design & data collection

Laboratory based observational study was conducted to explore antibiotic susceptibility patterns among all *K. pneumoniae* isolates from a tertiary hospital for a duration of one year. During the period, the total of 6274 clinical samples was processed after taking ethical approval from the ethical committee of the institution. Samples were collected from different intensive care of MICU, SICU, IC-CU and PCTICU wards and included different sample types, such as urine, blood, pus, sputum and ET secretion. Data collection has been collected about, age & gender of the patients and a brief clinical and antibiotic history of illness.

Settings

The study was carried out in the Department of Microbiology, at Krishna Institute of Medical Sciences (KIMS), a tertiary care hospital, Hyderabad, Telangana.

Sample Size

The study comprised of a total of 6274 clinical samples obtained from various clinical samples (pus, blood, urine, ET secretion) received in Microbiology lab for culture & sensitivity testing.

Inclusion Criteria

All isolates which formed lactose fermenting mucoid colonies on MacConkey agar and further confirmed as *Klebsiella pneumoniae* by Vitek-2 Compact (Biomérieux) were included in the study.

Exclusion Criteria

Species of *Klebsiella* other than *Klebsiella pneumoniae* were excluded from the study.

Method

All samples were processed as per standard bacteriological techniques for aerobic cultures [13]. They were inoculated on to Blood agar and MacConkey agar plates and incubated at 37°C for 24-48 hours. Isolates of *Klebsiella* were identified by their colony morphology as it forms large domeshaped colonies on Blood agar and lactose fermenting mucoid colonies on MacConkey agar. Gram staining was performed on the growth obtained in positive cultures which showed Gram negative, short, plump, straight rods. Isolates were further identified to species level by Vitek-2 Compact (Biomérieux) using Gram negative identification cards (as per manufacturer's guidelines).

Antimicrobial sensitivity testing was also determined by same system using Vitek-2 AST N 280 cards. Antibiotic sensitivity results were interpreted as per CLSI guidelines [14].

Results

This Observational study was carried out to find out the burden of infections caused by *K. pneumoniae* in one year. Out of 6274 clinical samples were processed during the study period, 185 (2.94%) were *K. pneumoniae*. It was isolated highest in ET secretion samples 107(9.73%), followed by urine 37 (2.18%), pus 22(1.34%) and blood 19 (1.02%). Due to the COVID-19 control policies rate of the *K. pneumoniae* isolates drastically reduced from 25.9% in 2020 to 17.9% in 2022 throughout the world.

Identification of *K. pneumoniae*

The analysis of the antimicrobial susceptibility pattern of *K. pneumoniae* in different type of samples revealed that ET secretions were more prominent sample type to study the infection rate (Figure 1A). Throughout the duration of the study, the highest number of culture positives was identified in ET secretions (9.73%) and lowest in blood (1.02%) (Figure 1B). Among urine pathogens identified in the laboratory *K. pneumoniae* was the second most isolate after the E.Coli (Figure 1C). Blood & Pus pathogen identification also showed the same results (Figure 1D & 2A). Interestingly ET secretion and sputum sample observation showed that highest number of *K. pneumoniae* positives compared to other isolates and sample type (Figure 2B & 3).

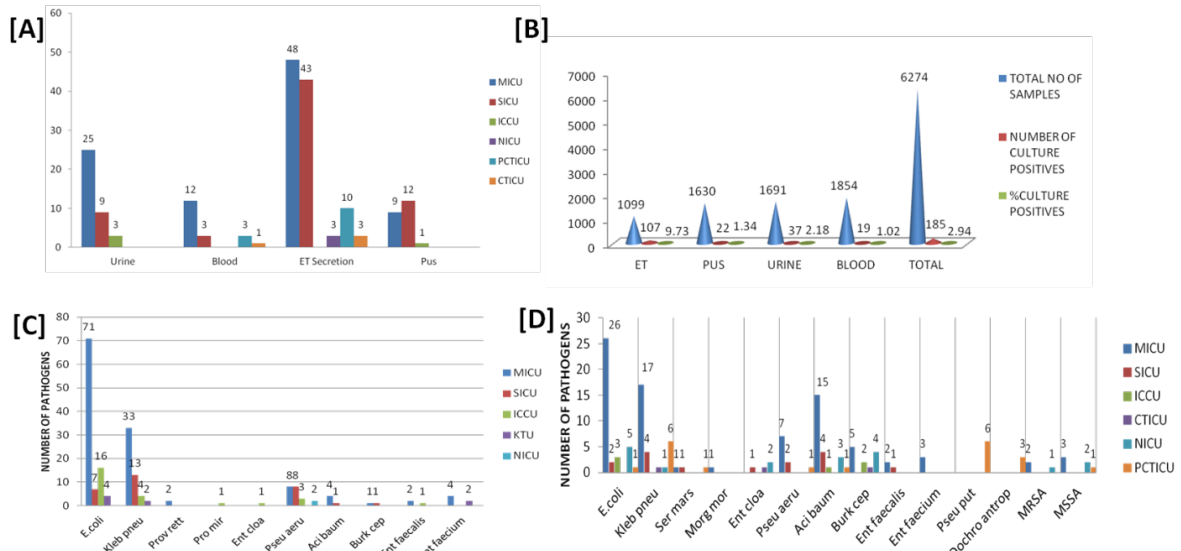


Figure 1: [A] Isolation of *klebsiella pneumoniae* according sample wise and ICU wise. [B] Culture positivity of *klebsiella pneumoniae* in various clinical samples. [C] Urine Pathogens. [D] Blood Pathogens

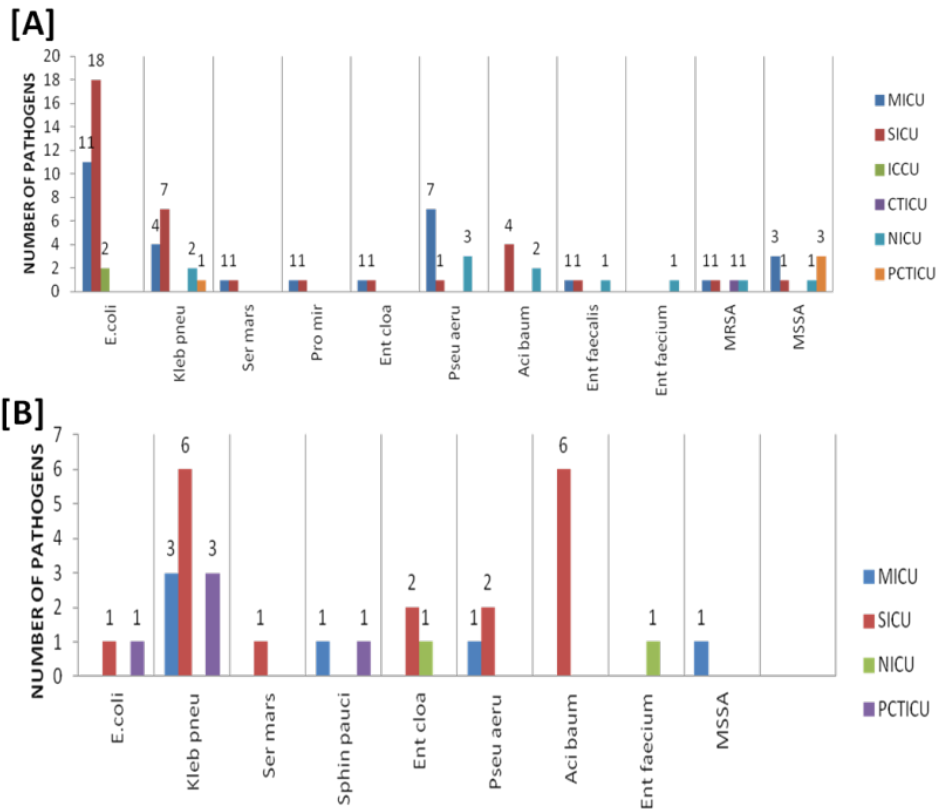


Figure 2: [A] Pyogenic Pathogens from Pus. [B] Pyogenic Pathogens from CLT

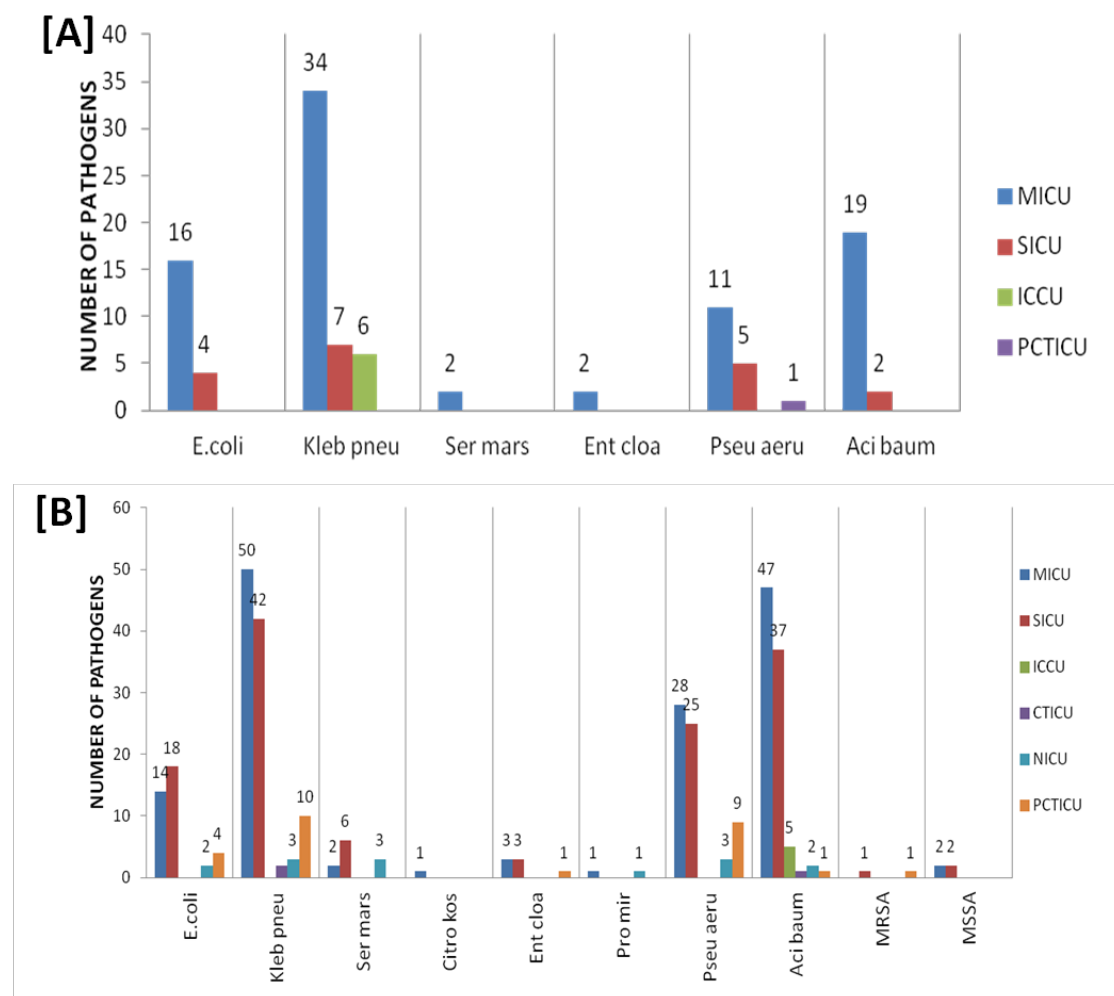


Figure 3: [A] Respiratory Pathogens from ET Secretion. [B] Respiratory Pathogens from Sputum

Antimicrobial Sensitivity Profile of *K. pneumoniae*

The Imipenem (IMI) and Meropenem (MERO) antibiotics showed a significant high sensitivity rate in Urine (79%) and ET secretion (55%) sample types and Tigecycline (TIG) antibiotic also showed increased sensitivity rate in ET secretion (66%), Pus (71%) and Blood (70%) sample type. Similarly, a sharp increase in sensitivity was observed for Amikacin (AK) in Urine (51%), ET

secretion (49%), Pus (57%) and Blood (52%) and for Ertapenem (ERT) in Urine (53%), ET secretion (47%), Pus (28%) and Blood (45%) sample. Nalidixic acid (NAL) and Nitrofurantoin (NIF) antibiotics were found sensitive in Urine pathogens.

Combined analysis showed significantly highest sensitivity for TIG (69%), MERO (63%), IMI (63%), AK (52%), ERT (43%) and gentamicin (GEN) (39%) (Figure 4 & 5).

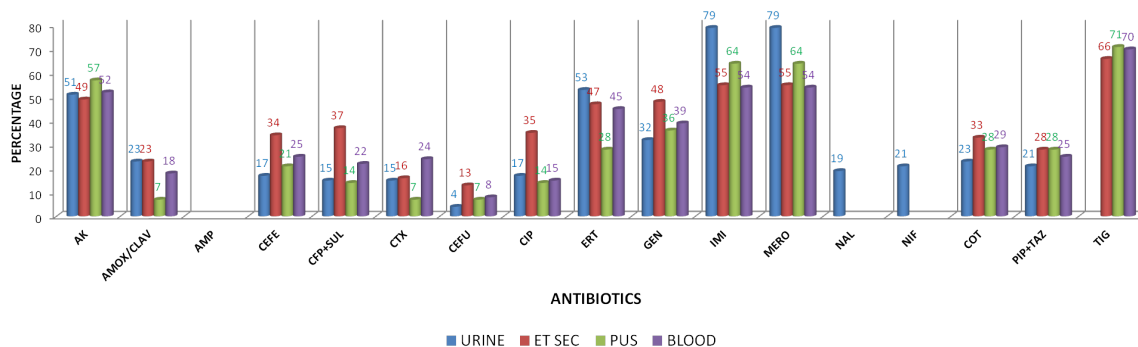


Figure 4: Antibigram in different sample types

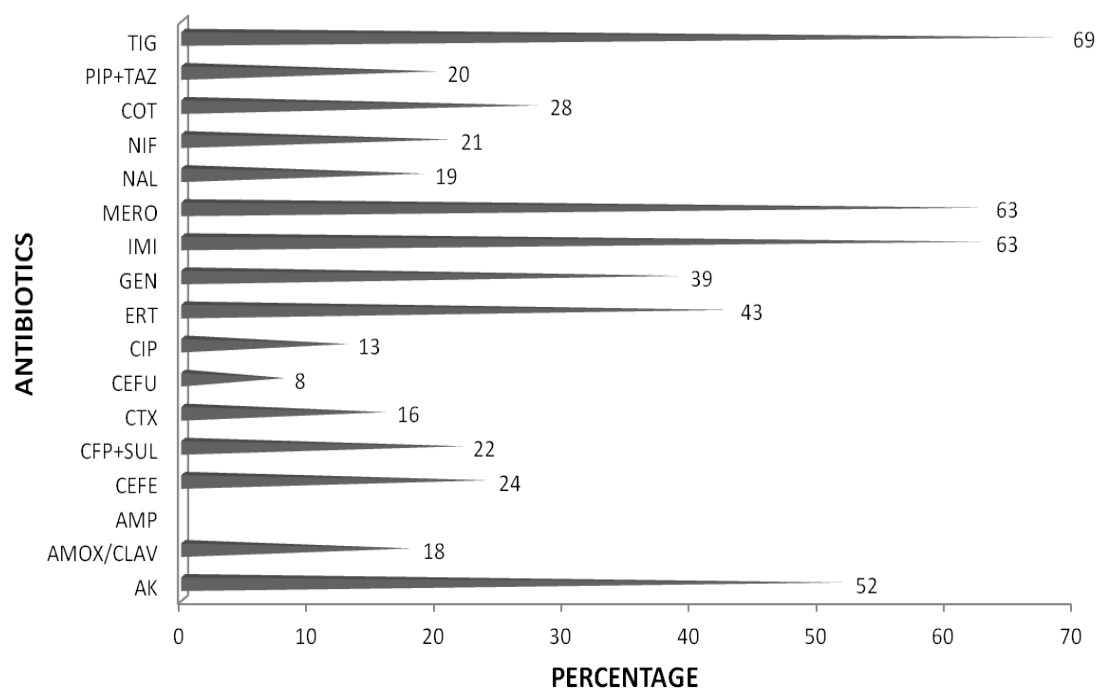


Figure 5: Percentage of Anti-biogram

Discussion & Conclusion

Klebsiella pneumoniae was the second most common pathogen isolated in our hospital from various clinical samples after *Escherichia coli*. It causes many nosocomial and community acquired infections like urinary tract infections, wound infections, septicemia, bacteremia and pneumonia. Antimicrobial resistance is a major problem all over the world to human health. Majority deaths cases could be avoided, if sensitive drugs can be replaced with resistant drugs [15].

Major AMR problem is arising from overdose and misuse of antibiotics [16 & 17]. Day to day *K. pneumoniae* multidrug resistance has been increasing with misuse and overdose of drugs and it leads to global emergence [18]. Therefore, AMR surveillance is most essential throughout the world. In India, very less number of studies was conducted for AMR monitoring to know the status of *K. pneumoniae*. Hence, our study was aimed to fill the gap by determining the isolation rate of *Klebsiella pneumoniae*, their antibiogram in various clinical samples in patients admitted in intensive care units of a tertiary care hospital.

Gill et al. observed that the highest percentage of *Klebsiella pneumoniae* isolated from pus (27.8%) followed by urine (22%), blood (8%) and sputum (8%) [19]. But, our study found ET secretion samples 107(9.73%), followed by urine 37 (2.18%), pus 22(1.34%) and blood 19 (1.02%). One most recent multicentre study from New Delhi performed prevalence and resistance pattern of uropathogens from community settings of different

regions and showed that 17.6% samples showed *K. pneumoniae* positivity out of 250 isolates. They observed that the resistance against nitrofurantoin (NIF) was dominated in the *K. pneumoniae* isolates in comparison to uropathogenic *E. coli* (UPEC) isolates [20]. However, our study also showed that NIF was found sensitive in Urine pathogens only.

In Conclusion, updated knowledge of the drug resistance pattern should be required for each and every region hospitals of the country, antibiotic stewardship program and following universal guidelines of hand washing techniques and continuous surveillance is vital in clinical practice to control and prevent the infections in intensive care units. Our study found that ET secretion sample type is the most prominent sample type.

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